

Chapter 1

Results

In this Chapter I present the results of applying the methodology explained in Chapter ?? to the Pleiades DANCe data set (Sect ??). However, to characterise the methodology and estimate its precision and accuracy, I first apply it over synthetic data. Using this data, I am able to analyse the performance of the methodology when it is considered only as a classifier. Later, in this Chapter I give the results of our methodology main objective: the statistical characterisation of the cluster population. In the following Sections I give the details of the spatial, velocity, luminosity and mass distributions. Later, I will describe the physical scenario of the evolution of the mass distribution by comparing the Pleiades mass distribution with other younger and older clusters. Finally, I will end this Chapter with a description of how the Bayesian methodology allowed us to update our previous knowledge of the Pleiades cluster.

1.1 Performance of the classifier

As mentioned earlier, the main objective of our the methodology of the BHM is the statistical characterisation of the NYOC populations. As a by product, it also obtains individual membership probability distributions. Using these last ones, we are able to directly classify objects into cluster and field members, providing that an objective probability threshold has been established. The objective of this section is to find this objective threshold by means of synthetic data. As any other measured property, this classification has an uncertainty, thus, the purpose of this

section is also to quantify this uncertainty.

That said, in order to properly characterise our classifier, I test it over synthetic data sets that resemble the real data. An ideal test to our classifier will be to apply it over well known dataset in which tags of cluster and field members were already present. However, if we may have access to these tags, a classifier may not be needed. The Pleiades cluster being *the* most studied cluster in history, is the NYOC with most of these tags. This is the reason for which we decided to benchmark our methodology on it. Nevertheless, the problem of the synthetic data remains since the low-mass end of the cluster still is *terra ignota*. To overcome this issue, we decided to create synthetic data sets under the assumption that our cluster and field models resemble the real data. We are aware that these models are far from perfect, but so far is the best we can do.

The assumption that our model correctly models the real data, although enable us to measure the uncertainty of our classifiers, does not give any indication about possible biases in our model. To explore this possibility, we later compare our real data results with those found in the literature. I present this comparison at the end of this section.

Hence, we fit our models, field and cluster, to the real data (10^4) and using the MAP estimates, we created synthetic stars (five samples of 10^4 objects each). To further test the reliability of our classifier, we compare the results it render when applied over data sets with and without missing values. This comparison allows us to quantify the impact that missing values have on our results.

One further consideration. The synthetic analysis requires at least three runs: one on the real data to obtain the MAP, and two on the synthetic one: with and without missing values. However, as explained in Chapter ??, our methodology is computationally expensive. Therefore, to maintain the computing time within reasonable limits (couple of weeks), we decided to restrict our synthetic data set to only the 10^4 objects with higher membership probability according to Bouy et al. (2015). I elaborate on the consequences of this decision.

These 10^4 objects are "closer" to the cluster in the sense of membership probability than the remaining 9×10^4 objects. Therefore, the field probability density rendered by this sample, compared to that of the larger 10^5 sample, has the following properties: it is more concentrated and has larger values near the cluster

region. Since the 10^5 sample is largely dominated by the field population, its density peaks far from the cluster proper motion and photometric sequences. Densities are normalised, thus more of the density mass of this large sample is far from the cluster region.

Given the previous considerations, we assume that results obtained on the smaller 10^4 sample have are more contaminated, and have lower recovery rates than those obtained on the larger and more distant 10^5 sample. On the one hand, the higher contamination rate results from the larger concentration of the field density around the cluster region. On the other hand, the lower recovery rates arises from the higher values of the field probability density. In simple words, when we define the field in a more restricted region around the cluster, both populations become more entangled, thus they become more difficult to separate. Therefore, we assume that the results obtained on the smaller 10^4 sample represent upper and lower limits to the contamination and recovery rates of the larger 10^5 sample, respectively.

Briefly, to create the synthetic data set, the procedure is the following. First, using the methodology of the previous Chapter, I obtain a sample of the posterior distribution of the parameters given the 10^4 real data set. Then, I chose the particle with highest posterior probability as the MAP estimate of the posterior distribution. Using this particle positions I generate five synthetic data sets of 10^4 objects each. Then, I tag these objects according to their parent population: cluster or field. Then, using the synthetically observed values I estimate their uncertainties and missing value patterns (more details below). Finally, I run the model over these five synthetic samples and compare the measured tags with the true ones as function of the probability threshold.

Also, I run the methodology over the synthetic data set without missing values and compare this results with those found on the same data set with missing values. This test, as mentioned before, enable us to quantify the impact of missing values over individual membership probabilities.

As explained in Sect. ??, our data set has a high fraction of missing values. Only $\sim 1\%$ has completely observed entries. Furthermore, the missing pattern is not random and depends on the magnitudes and colours of the objects. Therefore, to better reproduce this pattern, for each synthetic datum, we use missing value

template of one of its closer neighbours in the real data; closer in the euclidean sense. Using the missing value template of the nearest neighbour from the real data set results in a biased sample in which objects with complete (non missing) values are underestimated. This is the inevitable consequence of the fact that euclidean distances measured in subspaces resulting from the missing values, are smaller or, at most, equal to those measured in the non-missing value spaces.

Missing values are assigned as follows. Since by definition of our data set there are no missing values in our proper motion data, missing values were assigned only to photometry. We chose the closer neighbours from the available CMDs: $\{K_s, J - K_s\}, \{J, J - H\}, \{K_s, H - K_s\}, \{J, Y - J\}, \{K_s, i - K_s\}$. These CMD are formed with the bands and colours with fewer missing values, in decreasing order. The missing value pattern for individual objects was chosen as follows. First, for each CMD subspace we find the fraction, f_r , of objects from real data without missing values, we call it $C_{or,i}$. Then, we take a random sample from the synthetic data whose fraction, f_s corresponds to f_r . For objects in this sample we assign the missing value pattern of the nearest neighbour from sample $C_{or,i}$. We repeat the procedure for all CMDs. In this way, the synthetic data has fractions of missing and non-missing values similar to those of the real data.

Uncertainties are assigned as follows. We set the proper motions uncertainties to those of the nearest neighbour in the real data. IN photometry, however, this scheme renders uncertainties that are biased towards the less precise measurements. This is a consequence of the missing values. Again, the euclidean metric results in the preferential choosing of objects with missing values. These missing values occur mostly at the faint end, where uncertainties are larger. Therefore, the uncertainties are biased towards larger values. To avoid this issue, we fit polynomials (8th degree) to the uncertainties as a function of the magnitudes. Then, we use these polynomials to give uncertainties to the synthetic photometric data.

The performance of our classifier was measured by counting the true positives (TP, cluster members correctly classified), true negatives (TN, field members correctly classified), false positives (FP, field members classified as cluster members) and false negatives (FN, cluster members classified as field members) recoveries as a function of the probability threshold. With them we calculate the true positive rate, contamination rate, accuracy and precision, which are defined as follows. In

order to classify the objects as cluster of field members we summarise their membership probability distribution using the mode. If the mode is greater than the current probability threshold, then the object is classified as cluster member, if not as field.

The true positive rate (TPR) is the ratio of true positives over the sum of true positives plus false negatives. The contamination rate (CR) is the ratio of false positives over the sum of false positives plus true positives. The precision or positive predictive value (PPV) is the ratio of true positives over the sum of true positives plus false positives. Finally, the accuracy (ACC) is the ratio of the sum of true positives plus true negative over the sum of true and false positives and negatives. These are,

$$\begin{aligned} TPR &= \frac{TP}{TP + FN} \\ CR &= \frac{FP}{FP + TP} \\ PPV &= \frac{TP}{TP + FP} \\ ACC &= \frac{TP + TN}{TN + FN + TP + FP} \end{aligned}$$

We use the results of the five synthetic data sets to quantify the uncertainties of the previous quantities.

The left panel of Fig. 1.1 shows the TPR (solid lines) and CR (dashed lines) in the presence (red lines) and absence (blue lines) of missing values. Both quantities are measured as functions of the probability threshold. In the missing value case, the lines and the shaded grey regions depict the mean and deviations, respectively, of the results from the five synthetic data sets. As it is shown, the missing values have a negative impact in our classification process by diminishing the TPR and increasing the CR. Nevertheless, our methodology delivers low ($\lesssim 8\%$) contamination rates above the probability threshold $p \approx 0.75$. In this Fig. and for the sake of comparison, we also show the CR and TPR (as black dots) reported in Table 4 of Sarro et al. (2014). This Fig. shows that, the TPR of our methodology measured on data without missing values is similar to that of Sarro et al. (2014). This is expected since those authors use only completely observed objects

to construct their model. However, the TPR we measure on missing values data, at $p_t = 0.84$, is $\approx 4\%$ lower than that of Sarro et al. (2014) and the one we measure on non-missing values data. On the other hand, the CR of our methodology above $p = 0.8$ outperforms the CR reported by Sarro et al. (2014) in spite of the missing values in our data sets. Nonetheless, we stress the fact that this comparison is not straight forward because of the following reasons. First, Sarro et al. (2014) infer their cluster model using only non-missing-value objects, later they apply it over objects with and without missing values. Second, their synthetic data set and ours are essentially different. They are constructed with different generative models, different number of elements, and different missing value patterns.

The right panel of Fig. 1.1 shows the ACC and the PPV of our classifier when applied on synthetic data with missing values. The lines and the grey regions depict the mean and the maximum deviations of the results on the five synthetic data set. As this panel shows, the probability threshold with higher accuracy is $p_t = 0.84$. In what follows, and only for classification purposes, we use it as our cluster membership probability threshold. At this threshold the CR is $4.3 \pm 0.2\%$, the TPR is $90.0 \pm 0.05\%$, the ACC is $96.5 \pm 0.1\%$, and the PPV is $95.6 \pm 0.2\%$. The quoted uncertainties correspond to the maximal deviations from the mean of results in the five missing-values synthetic data sets.

Figure 1.1: Left: The TPR (solid line) and CR (dashed line) of our methodology when applied on synthetic data sets with and without missing values (red and blue lines, respectively). In black dots we show the TPR and CR reported by Sarro et al. (2014) for their non-missing values model. Right: Accuracy and precision as a function of probability threshold for our classifier when applied on synthetic data with missing values. The higher accuracy is obtained at $p_t = 0.84$ (red dot). In both panels, the grey areas show the maximum deviations from the mean of the results of the five missing-values synthetic data sets.

We investigate further on the impact of missing values. In Fig. 1.2 we compare the cluster membership probabilities we recover in the presence of missing values (vertical axis) to those without missing values (horizontal axis). As can be seen in this Fig., the missing values impact our results by spreading the membership probabilities. This spread is expected since in general, decisions are compromised

by the loss of information. The box (region above p_t) contains the objects which can be considered as the contaminants (at $p = p_t$) resulting from missing values. These objects have a small impact, representing only 1.8% of the contamination (indicated by the difference between the CR for missing and complete cases in left panel of Fig. 1.1 at p_t). The most striking difference between both probabilities comes from objects lacking the *CI* (enclosed in black). Our methodology uses the *true CI* to prescribe the *true* photometry, and the observed *CI* to constrain the marginalisation integral of the *true CI*. Thus, it is expected that a missing *CI* will produce a probability spread. These missing *CI* objects show two different behaviours. In one case, there are sources with membership probabilities $p_{complete} \approx 0$ which have overestimated probabilities in the incomplete case (vertical axis). In the other case, the sources in the combed area below the line of unit slope have underestimated probabilities in the incomplete case. While the first case contributes to the CR the second one diminishes the TPR. The first case reaches the maximum difference at $p \approx 0$ (difference between red and blue dashed lines in Fig. 1.1), thus its impact in our results is marginal. The second case, however, represents the unavoidable (in our model) loss of members due to the missing values (4% at $p_t = 0.84$). In future version we will try to diminish this breach. In spite of the mentioned behaviours, the root-mean-square (rms) of the difference between membership probabilities of both data sets (with and without missing values) is 0.12, which we consider an small price given the gained improvements due to the inclusion of missing values. This rms drops to only 0.02 for objects with completely observed values (red squares) in both data sets. The previous effects show an overall agreement between results on data sets with and without the missing values, nonetheless, care must be taken when dealing individually with objects lacking this colour index.

Finally, as explained in Sect. 1, our methodology aims at the statistical distributions of the cluster population. Our model returns these distributions without any threshold in cluster membership probabilities. In our methodology, each object contributes to the cluster distributions proportionally to its cluster membership probability. In this sense our results are free of any possible bias introduced by hard cuts in the membership probability. Nevertheless, contamination is still present and must be quantified. To quantify it, we compute the expected value of

the CR. It is $\langle CR \rangle = 5.8 \pm 0.2\%$. In it, each CR contributes proportionally to the probability threshold at which it is measured.

Figure 1.2: Comparison between the cluster membership probabilities recovered from the synthetic data with missing values (Incomplete) and without them (Complete). The colour and shape indicate the amount of missing values. The symbols enclosed in black indicate a missing *CI*. The top left box contains objects considered as contaminants due to missing values, at the probability threshold $p_t = 0.84$.

1.1.1 Comparison with the literature

1.1.1.1 Candidate members from Bouy et al. (2015)

The works of Bouy et al. (2015) and ours, although essentially different, have common elements which allow their comparison. In spite of the differences, both agree on $\approx 90\%$ of the recovered candidate members (the upper right corner of Fig. 1.3). In what follows, we detail the differences for individual objects.

In Fig. 1.3 we directly compare, for objects in our data set, the cluster membership probabilities recovered by both works. Although our results on the posterior distributions of the cluster population do not depend on this probability threshold, we use it here only to illustrate differences in the classification processes. As shown in this Fig., there is an overall outstanding, 99.6% agreement between both methodologies, which is shown by the upper right and lower left boxes of Fig. 1.3. Nonetheless, the differences are worthy of discussion.

The rejected candidates of Bouy et al. (2015) (lower right box of Fig. 1.3) amount to 12% of their candidate members. This value is higher than the contamination rate reported by Sarro et al. (2014), $7.3 \pm 1.4\%$. Also, the fraction of our new candidates (upper left box), 10%, is higher than the $4.3 \pm 0.2\%$ CR reported on Sect. ???. We plot the new candidates and the rejected ones of Bouy et al. (2015) in Figs. 1.4 and 1.5, respectively. In what follows we address these differences.

The new candidate members have proper motions uncertainties (median $\overline{\mu_{\alpha,\delta}} = \{1.33, 1.33\} \text{ mas/yr}$) two times larger than those of the candidate members in

common (median $\overline{\mu_{\alpha,\delta}} = \{0.65, 0.65\} \text{ mas/yr}$). Also, as shown by Fig. 1.4, the majority of them (148) have probabilities lower than 0.95, are located in a halo around the locus of the cluster proper motions and on top of the cluster sequence in the K_s vs $i - K_s$ CMD. On the contrary, the new candidates with probabilities higher than 0.95 (39), lay in the centre of the cluster proper motions and fall above the cluster sequence in the K_s vs $i - K_s$ CMD. Thus, we hypothesise that, i) objects with photometry compatible with the cluster sequence but in the proper motions halo, have higher membership probabilities in our methodology due to the increased flexibility of the cluster proper motions model (four gaussians instead of the two of Bouy et al. (2015)), and ii) objects at the centre of the cluster proper motions but above the cluster sequence are multiple systems (probably triple systems which can amount to 4% of the population Duquennoy & Mayor 1991) with an increased membership probability due to our more flexible photometric model of the cluster and equal-mass binaries sequences.

The rejected candidates of Bouy et al. (2015), as it is shown in Figs. 1.5 and 1.6, have proper motions uncertainties (median $\overline{\mu_{\alpha,\delta}} = \{3.15, 3.19\} \text{ mas/yr}$) more than four times larger than those of the candidates in common and are distributed along the cluster sequence. The relatively high membership probability among these objects occurs at the middle of the cluster sequence (green squares of Fig. 1.6) while the lowest probabilities occur at the bright and faint ends (blue and red triangles of Fig. 1.6, respectively), where the missing values happen the most. We stress the fact that Bouy et al. (2015) construct their field model using a sample of $\approx 20,000$ objects without missing values. Proceeding in that way underestimates the field density in the regions where missing values happen (see Fig. ??). Underestimating the field likelihood leads to an increase in the cluster field likelihood ratio, and therefore it increases the cluster membership probabilities. Furthermore, the proper motions uncertainties of objects at the bright end (median $\overline{\mu_{\alpha,\delta}} = \{4.0, 4.2\} \text{ mas/yr}$ and depicted as blue triangles), faint end (median $\overline{\mu_{\alpha,\delta}} = \{3.4, 3.4\} \text{ mas/yr}$ depicted as red triangles), and at the middle magnitudes (median $\overline{\mu_{\alpha,\delta}} = \{2.4, 2.4\} \text{ mas/yr}$ depicted as green squares) are approximately 6, 5 and 4 times larger than those of the candidates in common. Thus, we hypothesise that higher proper motion uncertainties and field likelihoods are responsible for our lower membership probabilities of Bouy et al. (2015) rejected

candidates. However, we stress the fact that, although the probability threshold $p_t = 0.84$ returns the maximum accuracy of our methodology, at this value the TPR is just $90.0 \pm 0.05\%$. Thus, the rejected candidate members of Bouy et al. (2015) cannot be discarded as potential members. To solve this controversy it is necessary to have lower proper motion uncertainties and fewer missing values. Future steps will be taken to try to solve this issue.

Finally, the discrepancies in the individual membership probabilities of both works, Bouy et al. (2015) and ours, arise from the subtle but important differences between them. The inclusion of missing values in our methodology have two main consequences. First, the use of missing values in the field photometric model leads to lower membership probabilities than those of Bouy et al. (2015) in the regions where missing values happen the most. Second, the use of missing values in the construction of the cluster model allow us to include the information of good candidate members that were otherwise discarded a priori. This last point, together with the higher flexibility of our cluster model allow us to rise the membership probability of the previously discarded candidates. Furthermore, as shown by the red squares in the upper left corner of Fig. 1.3, the higher flexibility of our cluster model allow us to include as new candidate members previously rejected objects with complete (non-missing) values.

Figure 1.3: Recovered membership probabilities compared to those of Bouy et al. (2015). Lines show the 0.75 and $p_t = 0.84$ probability thresholds used in both works. The numbers indicate the new candidate members (top left), rejected candidate members (bottom right), and common candidate members (top right).

Figure 1.4: Proper motion (left) and K_s vs. $i - K_s$ CMD (right) showing the new candidate members found in this work. Captions as in Fig. ??.

Figure 1.5: Proper motion (left) and K_s vs. $i - K_s$ CMD (right) showing the rejected candidate members of Bouy et al. (2015). Captions as in Fig. ??.

Figure 1.6: Proper motion (left) and K_s vs. $i - K_s$ CMD (right) showing the rejected candidate members of Bouy et al. (2015). The colours and shapes are a proxy for their K_s magnitude.

1.1.1.2 Known members from Stauffer

1.2 Velocity distribution

1.3 Spatial distribution

1.4 Luminosity distribution

We derive the distributions of the apparent magnitudes J , H , and K_s using the posterior distributions of the parameters in our photometric model. Briefly, we do this by transforming the true CI distribution into the J, H, K_s distributions using the splines series and the intrinsic dispersion of the cluster sequence. The Appendix 1.4.1 describes in detail how we do this transformation.

1.4.1 Derivation of the magnitude distributions

To derive the J, H, K_s magnitude distributions, we use the distribution of the colour index, CI , and the cluster and equal-mass binaries photometric sequences (the spline series). We exemplify this derivation on the K_s band, but similar transformations apply to the rest of the bands. To obtain the distribution of K_s for the cluster objects, we introduce the colour index CI , as a nuisance parameter and then we marginalise it. Thus,

$$p(K_s|\boldsymbol{\theta}_c) = \int p(K_s, CI|\boldsymbol{\theta}_c) \cdot dCI = \int p(K_s|CI, \boldsymbol{\theta}_c) \cdot p(CI|\boldsymbol{\theta}_c) \cdot dCI.$$

The term $p(K_s|CI, \boldsymbol{\theta}_c)$ corresponds to the GMM modelling the distribution of CI (Eq. ??), while $p(K_s|CI, \boldsymbol{\theta}_c)$ is the probability of K_s given the CI and the cluster parameters $\boldsymbol{\theta}_c$. Since our photometric model takes into account the equal-mass binaries, we include them proportionally to their fraction, $(1 - \pi_{CB})$. Thus,

$$\begin{aligned} p(K_s|\boldsymbol{\theta}_c) &= \int [\pi_{CB} \cdot p_{Cs}(K_s|CI, \boldsymbol{\theta}_c) + (1 - \pi_{CB}) \cdot p_{Bs}(K_s|CI, \boldsymbol{\theta}_c)] \\ &\quad \cdot p_{CI}(CI|\boldsymbol{\theta}_c) \cdot dCI. \\ &= \pi_{CB} \int p_{Cs}(K_s|CI, \boldsymbol{\theta}_c) \cdot p_{CI}(CI|\boldsymbol{\theta}_c) dCI \\ &\quad + (1 - \pi_{CB}) \int p_{Bs}(K_s|CI, \boldsymbol{\theta}_c) \cdot p_{CI}(CI|\boldsymbol{\theta}_c) \cdot dCI. \end{aligned} \tag{1.1}$$

In this equation, Cs and Bs stand for cluster and equal-mass binaries sequences, respectively. The terms inside the integrals correspond to Equations ?? and ?. However, since here we focus only on the distribution of K_s , we marginalise the rest of the bands. Also, we change the integration limits to those of the truncated colour distribution ($CI_{min} = 0.8, CI_{max} = 8$). Finally, we obtain

$$\begin{aligned} p(K_s|\boldsymbol{\theta}_c) &= \pi_{CB} \int_{CI_{min}}^{CI_{max}} \left[\left[\sum_{i=1}^5 \pi_{CI,i} \cdot \mathcal{N}_t(CI|\mu_{CI,i}, \sigma_{CI,i}) \right] \right. \\ &\quad \cdot \left. \int_{\tilde{Y}, \tilde{J}, \tilde{H}} \mathcal{N}(\{CI, \tilde{Y}, \tilde{J}, \tilde{H}, K_s\} | \boldsymbol{\mathcal{S}}(CI, \boldsymbol{\beta}), \Sigma_{clus}) d\tilde{Y} d\tilde{J} d\tilde{H} \right] \cdot dCI \\ &+ (1 - \pi_{CB}) \int_{CI_{min}}^{CI_{max}} \left[\left[\sum_{i=1}^5 \pi_{CI,i} \cdot \mathcal{N}_t(CI|\mu_{CI,i}, \sigma_{CI,i}) \right] \right. \\ &\quad \cdot \left. \int_{\tilde{Y}, \tilde{J}, \tilde{H}} \mathcal{N}(\{CI, \tilde{Y}, \tilde{J}, \tilde{H}, K_s\} | T_{Bs}(\boldsymbol{\mathcal{S}}(CI, \boldsymbol{\beta})), \Sigma_{clus}) d\tilde{Y} d\tilde{J} d\tilde{H} \right] \cdot dCI. \end{aligned}$$

The derivation of the J and H magnitude distributions is similar to the procedure described for K_s . We notice that, the derivation of these magnitude distributions takes into account the equal mass binaries and the systems which could have different mass ratios. Therefore, these distribution are the system magnitude distributions.

Then, we obtain the luminosity distributions using the magnitude distributions, the parallax and extinction of the cluster. We assume that the parallax is normally distributed with mean, 7.44 mas, and standard deviation 0.42 mas (Galli et al. 2017). This parallax distribution is convolved with the magnitude distributions to obtain the absolute magnitude distributions. Finally, we dereddened them employing the canonical value, $A_v = 0.12$ (Guthrie 1987), which we transform to the J, H, K_s values using the extinction law of Cardelli et al. (1989).

Since our methodology prescribes the *true* photometric quantities based on the *true* colour index CI , therefore, the completeness limits of this CI dictate those of the photometric bands. The upper completeness limits that Bouy et al. (2015) estimate for i and K_s are $i \approx 23$ mag and $K_s \approx 18$ mag (see their appendix A). As they also mention, due to the heterogeneous origins of the DANCe DR2 survey, its completeness is not homogeneous over its entire area. To overcome this issue, they identified a region, the inner three degrees of the cluster, with homogeneous spatial and depth coverage and restricted their sample to it. Here, instead of restricting the sample, we assume that the UKIDSS survey provides the homogeneous spatial coverage at the faint magnitudes, and quote more conservative completeness limits at the bright end. Figure 1.7 shows the K_s and i density for all sources in the Pleiades DANCe DR2. The upper completeness limits correspond to the point with maximum density, $i = 21.4$ mag, $K_s = 18.1$ mag. For the lower completeness limits we choose $i = 13.2$ mag and $K_s = 11.0$ mag because the density of brighter objects shows a sharp decline, probably due to saturation. Thus, we define the CI completeness interval as that of all the points, along the cluster sequence in the K_s vs. $i - K_s$ CMD, for which i and K_s are bounded by their upper and lower completeness limits, respectively. This results on $2.7 < i - K_s < 5.6$ mag. With it and the cluster sequence, we derive the completeness intervals for the J, H, K_s . Finally, we transform these intervals to absolute magnitudes and deredden them.

The luminosity distributions in J, H, K_s together with their completeness lim-

Figure 1.7: Density of all DANCe DR2 sources in K_s vs i magnitudes. Lines show our completeness limits, $13.2 < i < 21.4$ mag and $11 < K_s < 18.1$ mag. The grey area is considered incomplete.

its are depicted (orange lines, hereafter continuous HBM-Hierarchical Bayesian Model) in Fig. 1.8. For the sake of comparison we also show the luminosity distributions of: i) our candidate members ($p > p_t$) (black dashed line, hereafter discrete HBM), and, ii) the candidate members of Bouy et al. (2015) (blue dot-dashed line). We impute the missing values of the discrete cases using the nearest euclidean neighbour. The difference between the continuous HBM function and the discrete HBM comes from the imputed missing values and the objects used to obtain them. The continuous one uses all objects proportionally to their cluster membership probability while the discrete HBM uses only the high probability candidate members ($p > p_t$). We expect differences since the discrete HBM is not a random sample of the continuous HBM, therefore their distributions are not exactly alike. The differences between the discrete HBM and that of Bouy et al. (2015) arise mainly at the bright and faint end ($K_s \approx 4$ mag and $K_s \approx 11$ mag). We argue that the origin of these differences lay in our new candidate members and the rejected ones of Bouy et al. (2015) (as discussed in Sect. ??).

Figure 1.8: Luminosity functions from J, H, K_s (orange). Also shown the regions of incompleteness and the luminosity functions computed from: the candidate members of Bouy et al. (2015) (dot-dashed blue line), and our candidate members, ($p_{84\%} > p_t$, dashed black line).

1.5 Mass distribution

1.5.1 The mass-luminosity relation

1.5.2 Present day mass function

Now, we proceed to compare the photometric distributions of the cluster population to those present in the literature. First, we compute the present day system mass function (PDSMF) and compare it to the Initial Mass Functions (IMF) of Chabrier (2005) and Thies & Kroupa (2007). Then, we analyse and discuss the differences between the Pleiades PDSMF and those of the Trapezium and Hyades clusters.

We obtain the PDSMF, independently in the J, H, K_s bands, by transforming the luminosity functions into system mass functions using the mass-luminosity relations given by the BT-Settl models of Allard et al. (2012) (grid CIFIST2011bc for the 2MASS AB photometric system). Since the luminosity functions of Sect. ?? correspond to the luminosity of systems (single and binary stars), therefore the derived mass function is the system mass function. We assume an age of 120 Myr for the Pleiades together with solar metallicity. The transformation from luminosities to masses is proportional to the derivative of the mass-luminosity relation, and indeed very sensitive to it (see D’Antona 1998, for some words of caution). Therefore, we decide to fit the BT-Settl grid with splines, and obtain the derivatives from this fit.

Figure 1.9 shows the logarithmic PDSMF (ξ_L) for the J, H, K_s bands normalised on the completeness limits of the survey (see Sect. ??). This figure also shows, the PDSMF proposed by Bouy et al. (2015) (blue dashed line) and, the IMFs of Thies & Kroupa (2007) and Chabrier (2005). For this last one, we show its standard uncertainty (taken from Chabrier 2003) as a sample of blue lines. As shown in this Fig., the PDSMFs of this work compare well with each others, and, in the overlap interval, with the one proposed by Bouy et al. (2015). However, the difference that these PDSMFs show above $0.3M_\odot$ ($-0.5 < \log M/M_\odot$) may have its origin on the new and rejected candidate members. Particularly the new candidate members which are preferentially M stars (with masses in the range $0.075 - 0.6M_\odot$ or $-1.12 < \log M/M_\odot < -0.22$). Also, similarly to what Bouy

et al. (2015) pointed out, there is a possible flattening in the PDSMF below $50M_{Jup}$ ($\log M/M_{\odot} < -1.3$). However, due to the level of uncertainty in this region we have not enough evidence to claim it.

Using *PyMultiNest* (Buchner et al. 2014), we fit three models to our K_s band PDSMF in the completeness interval: a log-normal distribution and two power-law distributions, $m^{-\alpha}$, with two and three segments. Table 1.1 show the parameters of these models together with their evidence. Judging by the evidence the best fit is the two segment power-law distribution (solid black line in Fig. 1.9). This distributions is similar to that found by Bouy et al. (2015), except for the flat part in the low-mass range and the less steep slope in the high mass range. However, it is in clear discrepancy with the IMFs of Chabrier (2005), ($m_c = 0.25^{+0.021}_{-0.016}$ and $\sigma = 0.55^{+0.05}_{-0.01}$, the uncertainties are those reported by Chabrier 2003, for single objects) and of Thies & Kroupa (2007). The discrepancy between IMFs and PDSMFs may have its origin either on the not yet established uncertainties in the mass-luminosity relationships, on dynamical effects associated with age, or on both of them.

Table 1.1: Parameters and evidence of models fitted to the PDSMF

Model	Parameters	Log Evidence
LogNormal	$m_c = 0.36 \pm 0.03$ $\sigma = 0.46 \pm 0.02$	18.1 ± 0.1
Two Segments	$\alpha_0 = -0.11 \pm 0.06 \quad m \in [0.04, 0.22 \pm 0.01]$ $\alpha_1 = 1.13 \pm 0.1 \quad m \in [0.22 \pm 0.01, 0.56]$	2222.7 ± 0.4
Three Segments	$\alpha_0 = -0.05 \pm 0.6 \quad m \in [0.04, 0.08 \pm 0.03]$ $\alpha_1 = -0.1 \pm 0.1 \quad m \in [0.08 \pm 0.03, 0.22 \pm 0.01]$ $\alpha_2 = 1.13 \pm 0.1 \quad m \in [0.22 \pm 0.01, 0.56]$	2221.2 ± 0.3

Our PDSMF allows us to give a lower limit to the mass of the cluster. The mean mass of the cluster, in our entire mass range, is $0.26 \pm 0.006 M_{\odot}$. We compute the expected number of cluster members as the integral, over the whole range of membership probabilities, of number of objects at each membership probability, and its value is 3116 ± 110 objects. The product of the mean mass times the expected number of members is $807^{+38}_{-29} M_{\odot}$. Since we still lack the high mass range

of the PDSMF, this value is a lower limit to the mass of the cluster. However, we can not claim further on our results. The quoted uncertainties are underestimated since they do not take into account the uncertainties in the mass-luminosity relations, which are yet to be established.

Figure 1.9: Normalised PDSMF in J, H, K_s bands. Also shown the IMFs of Chabrier (2005); Thies & Kroupa (2007) and fits to the PDSMF found by us and Bouy et al. (2015).

1.6 The mass distribution on time

Dynamical effects may have an impact on the cluster mass function. Figure 1.10 (left panel) compares the PDSMF from the Pleiades (≈ 120 Myr) derived here, to those of the Trapezium (≈ 1 Myr) and Hyades (≈ 600 Myr). These PDSMFs correspond to those of Fig. 11 of Bouy et al. (2015) (private communication). As mentioned by Bouy et al. (2015), the abundance of low-mass stars and brown dwarfs in the range $0.03 - 0.1 M_\odot$ ($\log M/M_\odot \approx \{-1, -1.4\}$) seems to diminish with time (since the PDSMF is normalised, this produces a relative increase of low-mass stars in the range $-0.4 < \log M/M_\odot < -0.2$). This effect is consistent with the classical scenario in which low-mass stars and brown dwarfs are ejected as the cluster relaxes. To test the validity of this scenario, at least the statistical significance of the observed differences among the PDSMF of this three clusters, we test the null hypothesis that the Trapezium and the Hyades have the same PDSMF as the Pleiades. Since we just have the cluster model of the Pleiades, we are not able to perform model comparison in a bayesian fashion. Thus, to do the statistical comparison of these three clusters PDSMF we use the Kolmogorov-Smirnov and Anderson-Darling tests.

The right panel of Fig. 1.10 shows the cumulative distribution functions (CDFs) of the Trapezium, Pleiades (only in K_s band) and Hyades PDSMFs. Also and for comparison, we show the CDFs of Chabrier (2005) and Thies & Kroupa (2007) IMFs. The grey area around the Pleiades CDF shows the hypothesis test in which we compare each CDF with that of the Pleiades. The null hypothesis is that each

Figure 1.10: Left: PDSMFs of the Pleiades (derived here for J, H, K_s bands), Trapezium, and Hyades, from Bouy et al. (2015). They are normalised in the interval of completeness. Right: Cumulative distribution functions (CDF) of the PDSMFs from left panel and that of Chabrier (2005) and Thies & Kroupa (2007) system initial mass function (normalised also in the interval of completeness). The Pleiades CDF shown is just from K_s band. The grey area depicts the area in which the null hypothesis of same PDSMF as that of the Pleiades can not be rejected (at $\alpha = 0.01$).

compared CDF is exactly that of the Pleiades. We use the Kolmogorov-Smirnov statistic and the alpha value $\alpha = 0.01$, to compute the vertical distance d_α from the Pleiades CDF, the grey region. The null hypothesis is rejected only if the tested CDF lies entirely outside the grey region around the Pleiades CDF. As can be seen, neither the IMFs nor the PDSMF of the Trapezium and Hyades lay entirely within the grey area, thus we can reject the null hypothesis that they share the same PDSMF of the Pleiades. Furthermore, since the Kolmogorov-Smirnov test uses only the maximum distance between CDFs, we also applied the more robust Anderson-Darling test. It also rejects the null hypotheses (at $p < 0.004$) that the Trapezium and Hyades PDSMFs and the Chabrier (2005) and Thies & Kroupa (2007) IMFs have the same CDF of the Pleiades.

The previous tests show that there is enough evidence to claim for differences among the PDSMFs of these three clusters and from IMFs and Pleiades PDSMF. Thus suggesting that these differences may have an origin on dynamical effects associated with age and relaxation. Nevertheless, to claim for reliable evidence supporting these differences the census of the Trapezium and Hyades must be done using the same methods. Also, the uncertainties must be properly establish both for the other PDSMFs and for the mass-luminosity relation from which all these PDSMF are derived.

1.7 Updating the previous knowledge

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